

FIG. 1

GENETIC MARKERS, STSs,  
 AND RECOMBINANTS

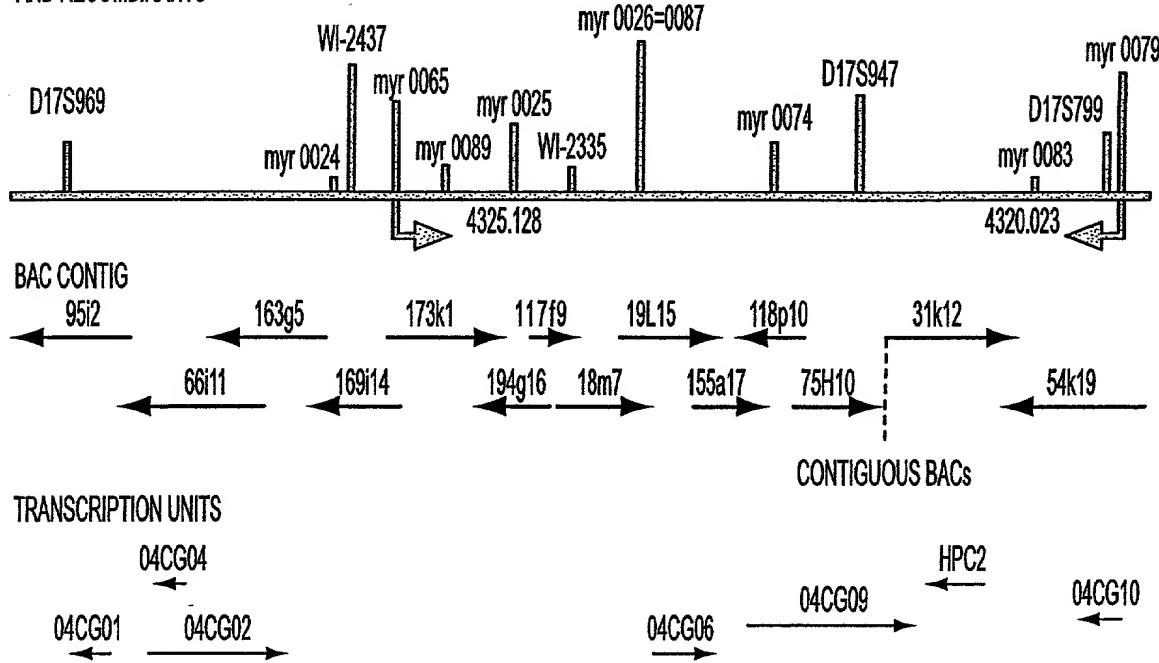


FIG. 2A

BAC 31k12 WITH 2 EXONS OF 04CG09 AND THE HPC2 TRANSCRIPTION UNIT

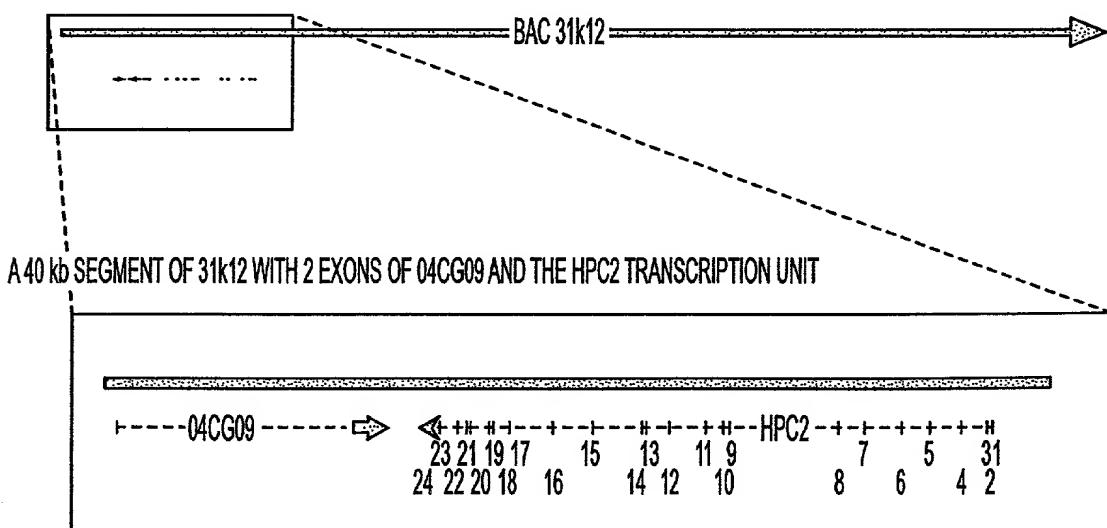


FIG. 2B

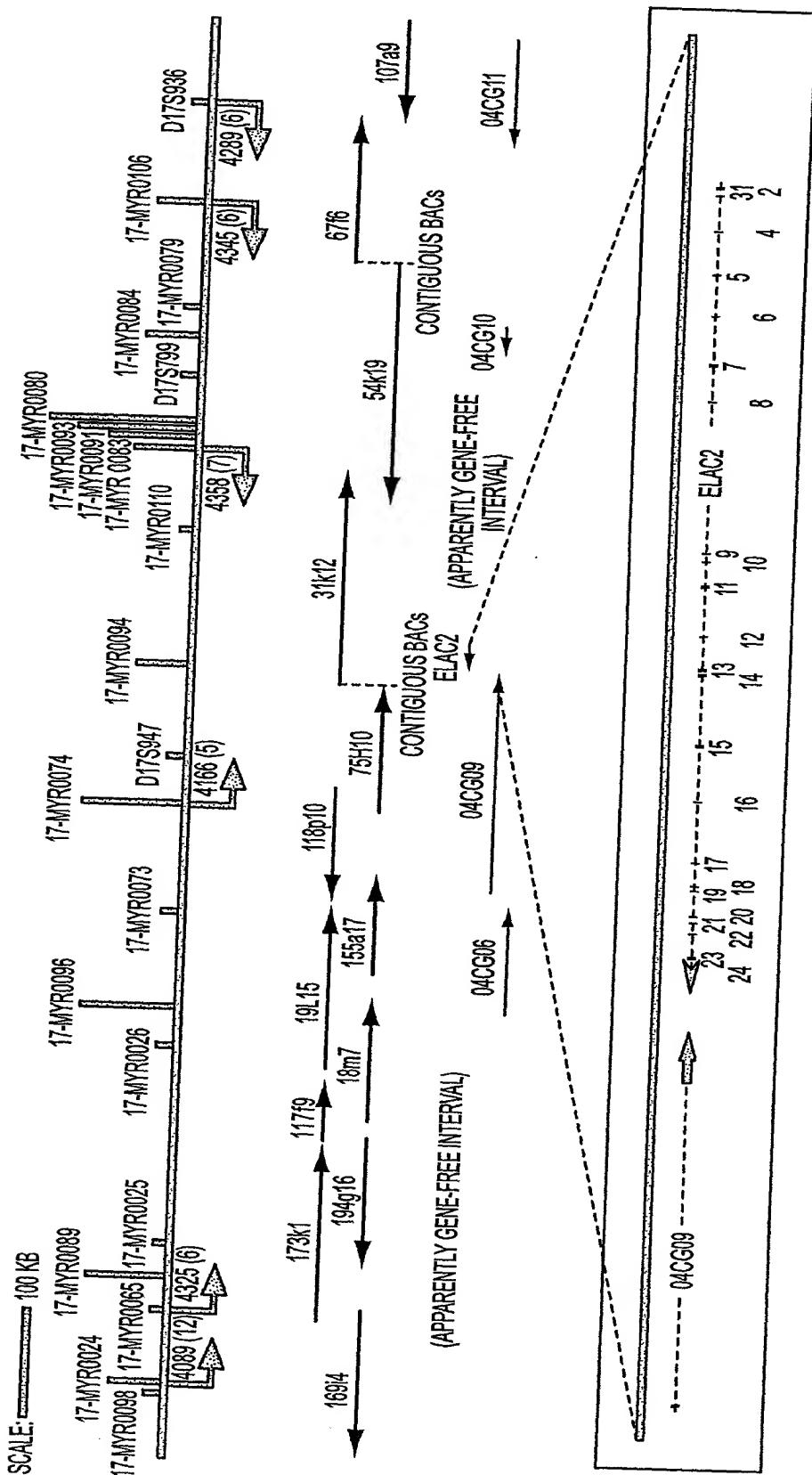


FIG. 3

Hs.HPC2.exon1	cgcgccgttaggtaccggcggtttctcagtttggtgagacggcgc
Hs.HPC2.exon1.pep	
Mm.HPC2.exon2	tggcgccgtgagggtctggctgccttgtcagcctggtgtggcgggtgc
Mm.HPC2.exon1.pep	
----- ----- ----- ----- -----	
	1 11 21 31 41
Hs.HPC2.exon1	ATGTGGGCGCTTGCTCGCTGCGTCCGGCCGGACGCACCATGTC
Hs.HPC2.exon1.pep	M-W-A-L-C-S-L-L-R-S-A-A-G-R-T-M-S-
Mm.HPC2.exon2	ATGTGGGCGCTCCGCTACTGTTGCGTCCCGCTGGCCTGCGCACCATGTC
Mm.HPC2.exon1.pep	M-W-A-L-R-S-L-L-R-P-L-G-L-R-T-M-S-
----- ----- ----- ----- -----	
	51 61 71 81 91
Hs.HPC2.exon1	GCAGGGACGCACCATATCGCAGGCACCCGCCGCCGAGCGGCCGCA
Hs.HPC2.exon1.pep	-Q-G-R-T-I-S-Q-A-P-A-R-R-E-R-P-R-K
Mm.HPC2.exon2	GCAGGGT-----TCGGCTCGTCGGCCGCGGCCACCCA
Mm.HPC2.exon1.pep	-Q-G-----S-A-R-R-P-R-P-K
----- ----- ----- ----- -----	
	101 111 121 131 141
Hs.HPC2.exon1	AGGACCCGCTGGCACCTGCGCACGCGAGAGAAGCGCGGACCGTCGGG
Hs.HPC2.exon1.pep	--D-P-L-R-H-L-R-T-R-E-K-R-G-P-S-G-
Mm.HPC2.exon2	AAGACCCACTGCGACACCTGCGTACGCGGGAGAAGCGCGGCCGGT--
Mm.HPC2.exon1.pep	--D-P-L-R-H-L-R-T-R-E-K-R-G-P-G--
----- ----- ----- ----- -----	
	151 161 171 181 191
Hs.HPC2.exon1	TGCTCCGGCGGCCAACACCGTGTACCTGCAGGTGGTGGCAGCGGGTAG
Hs.HPC2.exon1.pep	C-S-G-G-P-N-T-V-Y-L-Q-V-A-A-G-S-
Mm.HPC2.exon2	---CCGGGGGCCGAACACCGTGTACCTGCAGGTGGTGGCGGCCGG
Mm.HPC2.exon1.pep	---P-G-G-P-N-T-V-Y-L-Q-V-V-A-A-G-G-
----- ----- ----- ----- -----	
	201 211 221 231 241
Hs.HPC2.exon1	CCGGGACTCGGGCGCCGCGCTCTACGTCTCCGAGTTCAACCGgtcag
Hs.HPC2.exon1.pep	-R-D-S-G-A-A-L-Y-V-F-S-E-F-N
Mm.HPC2.exon2	CCGGGACGCCGGGCTGCTCTATGTTCTCGGAATACAACAGgtcag
Mm.HPC2.exon1.pep	-R-D-A-G-A-A-L-Y-V-F-S-E-Y-N
----- ----- ----- ----- -----	
	251 261 271 281 291
Hs.HPC2.exon1	tcaacgagccacgccccgtcccgctggccctcagtgcggcgagcctct
Hs.HPC2.exon1.pep	
Mm.HPC2.exon2	agtggccgacagccctggggattggcccccagcgccacgtgctcgggag
Mm.HPC2.exon1.pep	
----- ----- ----- ----- -----	
	301 311 321 331 341

FIG. 4

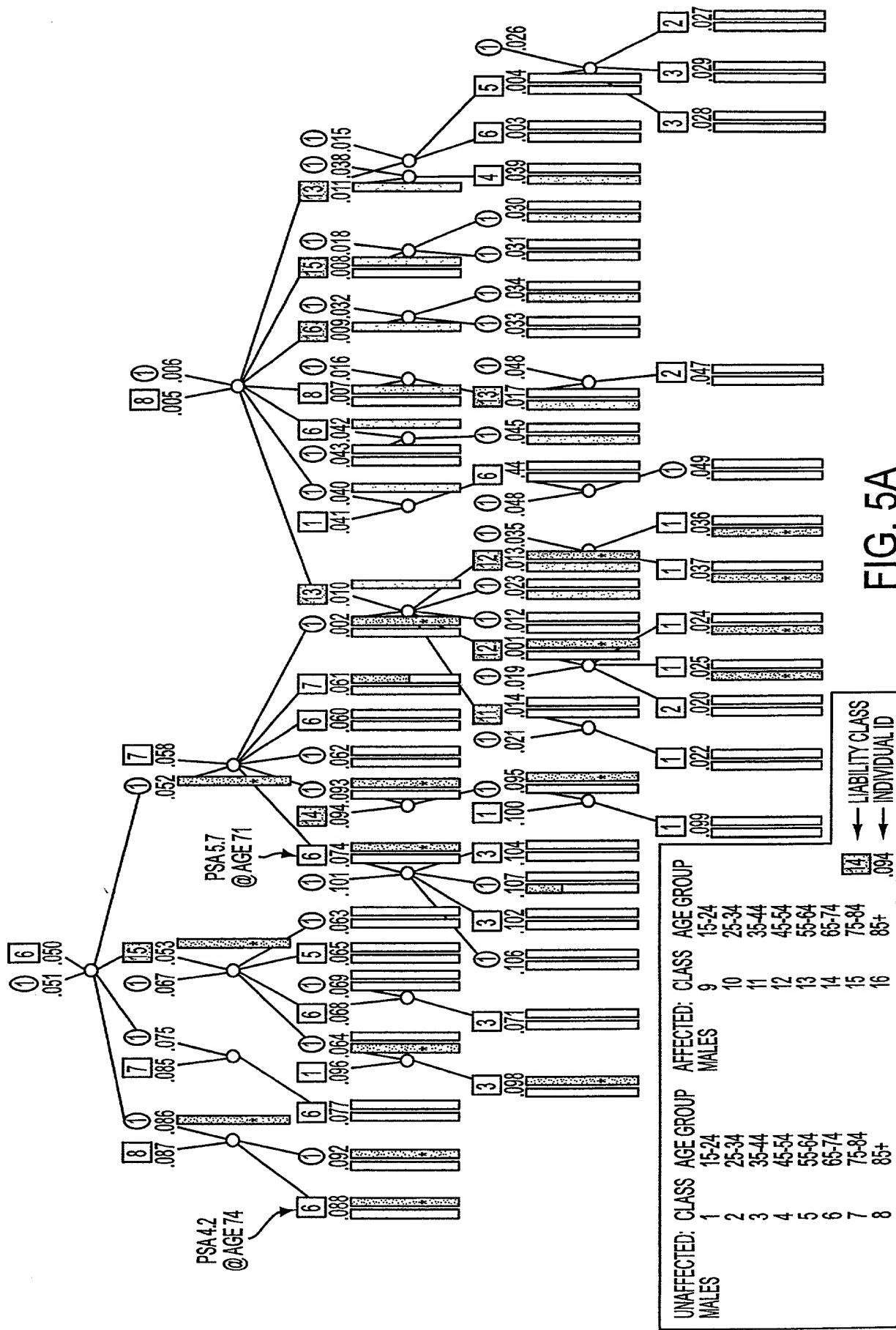


FIG. 5A

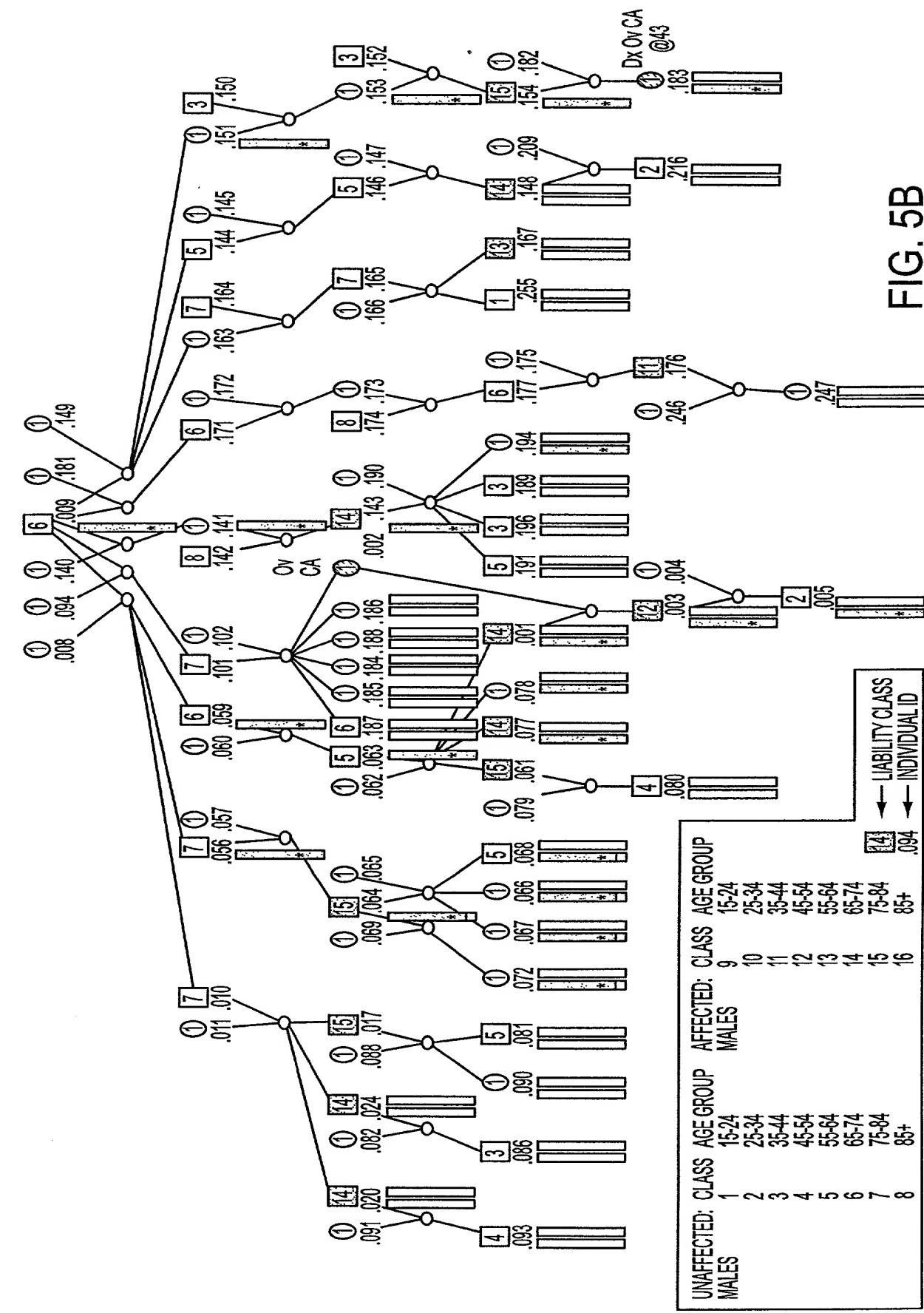


FIG. 5B

FIG. 6A-1

(HSA) Blac2 401 ... TSEFCKKEGPTLSVPMVQCECLKYQLPRREWQR. .... DAIITCNPEEFIVEAL... QLPNFQQSVQYRRSAQDG.  
 (MMU) Blac2 397 ... TSFYSKEEGSTLSVTPTRGECLKYQLPKREWQR. .... DTTLDCTDEFIAEAL... ELPDFQESVEYRKVNQEN.  
 (CEL) CE16965 407 ... HPIDWSGLITQTQNEELSQRODQFIRV.APMQRYWMR. .... RGA... SFNEEPIVNNLLAEEPELSDKAK. ELIKEYQK..  
 (ATH) gi6850339 374 RLNYLCQQFPAPGFWPSQLTDSIIIDPTPSNKE. NLRPVAIRGIDRSCIPAPLTSSEVDELLSEIPEIKDSSEEIKQFPIKQHNKTIEKWLSECNT  
 (SCE) YKR079C 362 YDRFDTPLSRGTSMSCKSQEEPIINTLIEKDNIHFSQNKTVTFPFRMNEEPMKCNINGEVADFSWQEEFEE. HVKPL. EPLLADVD. TVINNQLHVDN..

1641 ins G

(HSA) Blac2 471 ... PAPAEKRSQYPELIE LGTGSALPMKIRNVSATLNNISP... DTSLLIDCCEGCTEGQICRHIGDQ. VDRVLTGTAATGSI  
 (MMU) Blac2 467 ... PAPAEKRSQYPEIVF LGTGSALPMWIRNVSSSTLVNLSP... DKSVLVLDCEGCTEGQICRHIGQO. IDRVYLCSTAVFVSHLHADHHTGJLNI  
 (CEL) CE16965 475 ... LEKENKMDCEFFPLTTFGTSSAVPSKIRNVTG. YLVEASE... NSAILLIDVGEGTYGONRAVFGEDGCKQLLVNNINCWLVHADHHTGJLNI  
 (ATH) gi6850339 473 VLPNCLEKIRDDMELIVLIGTGSQPSKIRNVSASAEFIDIES... RGSLLIDCCEGCTLGQQLKRRYGLDGADEAATKARLCTIWISHI HADHHTGJLARI  
 (SCE) YKR079C 456 .FNNSAEKKKHVEIIT. LGTGSALPSKIRNVSITLVKVPFTDADGNTINRNIMLDAGENTLGTIRHMESQLAVKSIEQDQKMIYLSHLHADHHLGJISV

1641 ins G

(HSA) Blac1 1 MSNDVTP. LGTGAAYPSPTRGASAVVLRCE... GEOWLIDCCEGCTQI... MKSQLKAGRETKIPTITHHGDAFPFJLPGI  
 (Es c) elac 1 MKRDELMELIF LGTSGAVPTRTRNVTI. ILLNLQHPT... QSGIWLIDCCEGCTQHOL... LHATAFNPGRKDKEFISHLHGDHLEGLPGL  
 (Syn sp) gi2500943 1 MELTP. LGTSSGAVPTRNRMVSS. IAIIRLPO... RAEIWLFD CCEGCTQHOF... LRSEVVKISQI... TRIFITHHGDEHILGPGM  
 (Me t) gi2622965 1 MMEVTP. LGTSSGAVPSKMRNHTS. IAIIRIP... GEIILED CCEGCTQRM... ALAGISPAK... TRIFITHHGDEHILGPGM

FIG. 6A-2

(HSA) ELAC2	559	LLQPERALASLGKPLHPLWVAPNQLKAWLQOQHNCQEVLHISMIPAKCLOQEGAIISSPAVERLISSLLRTC	559	LLQPERALASLGKPLHPLWVAPNQLKAWLQOQHNCQEVLHISMIPAKCLOQGAEVSNITLERLISLLLET
(MMU) Elac2	555	LLQREHALASLGKPFQPLWVAPTQLRAWLQOQHNCQEVLHISMIPAKCLOQGAEVSNITLERLISLLLET	555	LLQREHALASLGKPFQPLWVAPTQLRAWLQOQHNCQEVLHISMIPAKCLOQGAEVSNITLERLISLLLET
(CEL) CE16965	565	IAARRKEAFESLGAPIRPLWVCNRNLVKPMLKTYISICPENIEHLLIEDISRYPLTPGSPGGPPGKPRPLSPHLPSSRDLVQDM	565	IAARRKEAFESLGAPIRPLWVCNRNLVKPMLKTYISICPENIEHLLIEDISRYPLTPGSPGGPPGKPRPLSPHLPSSRDLVQDM
(ATH) gi 68500339	564	LAU · RSKLLKGVTHEPVIVVGPRLKRFELDAYQRRLLEDLMEPLDCRSTTATSWASLESGEAEGLSLFTQ · GSPMQSVFGRSDIISMDNSSLVLC · LK	564	LAU · RSKLLKGVTHEPVIVVGPRLKRFELDAYQRRLLEDLMEPLDCRSTTATSWASLESGEAEGLSLFTQ · GSPMQSVFGRSDIISMDNSSLVLC · LK
(SCE) YKR079C	554	L · NEWYKYNKDDETSYVWVTPWQVHKFVNENL · VLENKEILKRIKYISCEHFINDSFVRMQTQSVPLAEFNEILKENSNQESNRKLELDRSSYRVDV	554	L · NEWYKYNKDDETSYVWVTPWQVHKFVNENL · VLENKEILKRIKYISCEHFINDSFVRMQTQSVPLAEFNEILKENSNQESNRKLELDRSSYRVDV
(HSA) ELAC1	75	TC · TISI0SGSMVSKQPIEIVPGVGLRDFWRTMELSHTELYVHYVV · HELVPTADQCPAELKEFAHNVRADS · · · · ·	75	TC · TISI0SGSMVSKQPIEIVPGVGLRDFWRTMELSHTELYVHYVV · HELVPTADQCPAELKEFAHNVRADS · · · · ·
(Es_c) elac	83	TC · · · · · CSRSMGIIQPLTLYPGQGIREFVETAL · · · · ·	83	TC · · · · · CSRSMGIIQPLTLYPGQGIREFVETAL · · · · ·
(Syn_sp) gi 25000943	75	TC · · · · · ASSGLAGSGQGIEIYGPBGLGDDYLEACC · · · · ·	75	TC · · · · · ASSGLAGSGQGIEIYGPBGLGDDYLEACC · · · · ·
(Me_t) gi 2622965	74	TC · · · · · QSMGFRGRREEPLDIYGPGLHELHECTIN · · · · ·	74	TC · · · · · QSMGFRGRREEPLDIYGPGLHELHECTIN · · · · ·
(HSA) ELAC2	633	TC · · · · · DEEEFOTCLVRECKH · · · · ·	633	TC · · · · · DEEEFOTCLVRECKH · · · · ·
(MMU) Elac2	629	TC · · · · · DEEEFOTCLVRECKH · · · · ·	629	TC · · · · · DEEEFOTCLVRECKH · · · · ·
(CEL) CE16965	650	TC · · · · · SSSFDKKKAWKLDDELKAVQVHTRMANGFVMVR · · · · ·	650	TC · · · · · SSSFDKKKAWKLDDELKAVQVHTRMANGFVMVR · · · · ·
(ATH) gi 68500339	657	TC · · · · · NLKVVLSEIGLNDLISFPVWECPQAYGVVVIKAER · · · · ·	657	TC · · · · · NLKVVLSEIGLNDLISFPVWECPQAYGVVVIKAER · · · · ·
(SCE) YKR079C	651	TC · · · · · LIRMYEDISIEYFOTCRAIECDW · · · · ·	651	TC · · · · · LIRMYEDISIEYFOTCRAIECDW · · · · ·
(HSA) ELAC1	163	TC · · · · · NSVLLFDEEQEV · VKAFFRLHRIPSFGFSVVEKKRPGKLMQKIKLQVPGPAYGKLNKGISVVLENGVTISPODVLKKPPIVGRKICIEGDCSC · VVGD	163	TC · · · · · NSVLLFDEEQEV · VKAFFRLHRIPSFGFSVVEKKRPGKLMQKIKLQVPGPAYGKLNKGISVVLENGVTISPODVLKKPPIVGRKICIEGDCSC · VVGD
(Es_c) elac	130	TC · · · · · GEILDDGLRK · VTAYPELHPLECYVRIEEHDKGALMQAIIKAAGVPPGPLFQELKAGKTITLEDGRQINGADYLAAAPPGKALIAFGDTGP · CDAA	130	TC · · · · · GEILDDGLRK · VTAYPELHPLECYVRIEEHDKGALMQAIIKAAGVPPGPLFQELKAGKTITLEDGRQINGADYLAAAPPGKALIAFGDTGP · CDAA
(Syn_sp) gi 25000943	122	TC · · · · · N · GLIYEDKDFQ · VHCGLLKHRIPAYGVIRVEEKQRPGRNTEQBALGICPPGPIYGOLQKGKTVTLEDGRRIRGQDLCPEDEPGRKEVYCTDTVF · CEEA	122	TC · · · · · N · GLIYEDKDFQ · VHCGLLKHRIPAYGVIRVEEKQRPGRNTEQBALGICPPGPIYGOLQKGKTVTLEDGRRIRGQDLCPEDEPGRKEVYCTDTVF · CEEA
(Me_t) gi 2622965	121	TC · · · · · G · TVV · EDDYR · VTSAPASHESVNLAYCSEEKKRPR · FIREKAIAGLKPKPAFKLHRGIPVVRGD · RIIMPEEVILGSPRKGVWVCKYISGDTD · CESV	121	TC · · · · · G · TVV · EDDYR · VTSAPASHESVNLAYCSEEKKRPR · FIREKAIAGLKPKPAFKLHRGIPVVRGD · RIIMPEEVILGSPRKGVWVCKYISGDTD · CESV

FIG. 6B-1

(HSA) ELAC2	674	VRMGK · DATLLIHEATLEDGL ·	670	SPNFS EKVGVAEDDM	
(MMU) Elac2	670	VQMGK · DATLLIHEATLEDGL ·	670	SPD FNEKVGIAEDDM	
(CEL) CE16965	699	VEEGK · DADVLVHEATLEDGL ·	699	PEYLD KENIGVAMDM	
(ATH) gi68500943	711	VEASR · DATLLIHEATLEDGL ·	711	ESHMWHNTCLIAEDDM	
(SCE) YKR079C	708	SLEIGY · NSDLLIHEATLENQL ·	708	NNIDVMAREFCFAEDDM	
(HSA) ELAC1	261	GGVKLCPEADLILHEATLDDAQ ·	226	MDKAK EHGHSIPQMAATFAKLCKRKLW ·	
(Es_c) elac	226	LDLAK · GVDVMMVHEATLDITM ·	226	MDKAK EHGHSIPQMAATFAKLCKRKLW ·	
(Syn_sp) gi2500943	219	IALAQ · EADLILHEATFAHQD ·	219	EAKANSRGHSISSTROQATLAREAGVGLL ·	
(Me_t) gi2622965	215	IKLAE · GAEELIHESTLEAGS ·	215	AQIAFDRHLHSTSTMAAQVALLANVKQJLW ·	
(HSA) ELAC2	751	XIVYCEPDEPTMPKLIPPLKALFAGDIEMEERERKRELQWRAALLSRELAGGLEDGEPOQQKRAHTEPOAKKVRAQ	747	▼R781	
(MMU) Elac2	747	KVCEFGDEPTVPLKIPPLKALFAGDIEMEERERKRELQWRAALLTQQ · ADSPEDREPOQQKRAHTEPHSPQSQQKESVANTLGARV	794	▼R781	
(CEL) CE16965	794	RTREDHPLPLVSKLPLIPREVFAELFELTIKEQRVILDKELSEKRGQQLKA	794	SLMMADLHLVLPKVLPYFKTLERDEMVEDADDVANDDKEEAL	
(ATH) gi68500943	794	INDYERKIGEQQRIFPLINKAEEKEEEEDDDVYESTQDIEVKLKKKKN	789	EDQEVYIJAEDENVISIPIKK	
(SCE) YKR079C	789	344	304	300	291
(HSA) ELAC1	344	DIQEVYIJAEDENVISIPIKK	304	NDP · TENV	
(Es_c) elac	304	300	300	RDF · LTWEIPRRTADPAIAMSTPQASPA	
(Syn_sp) gi2500943	300	291	291	DDL · MTVEVKAYDSSPDS	
(Me_t) gi2622965	291	291	291	DDL · MTVEVKAYDSSPDS	

FIG. 6B-2

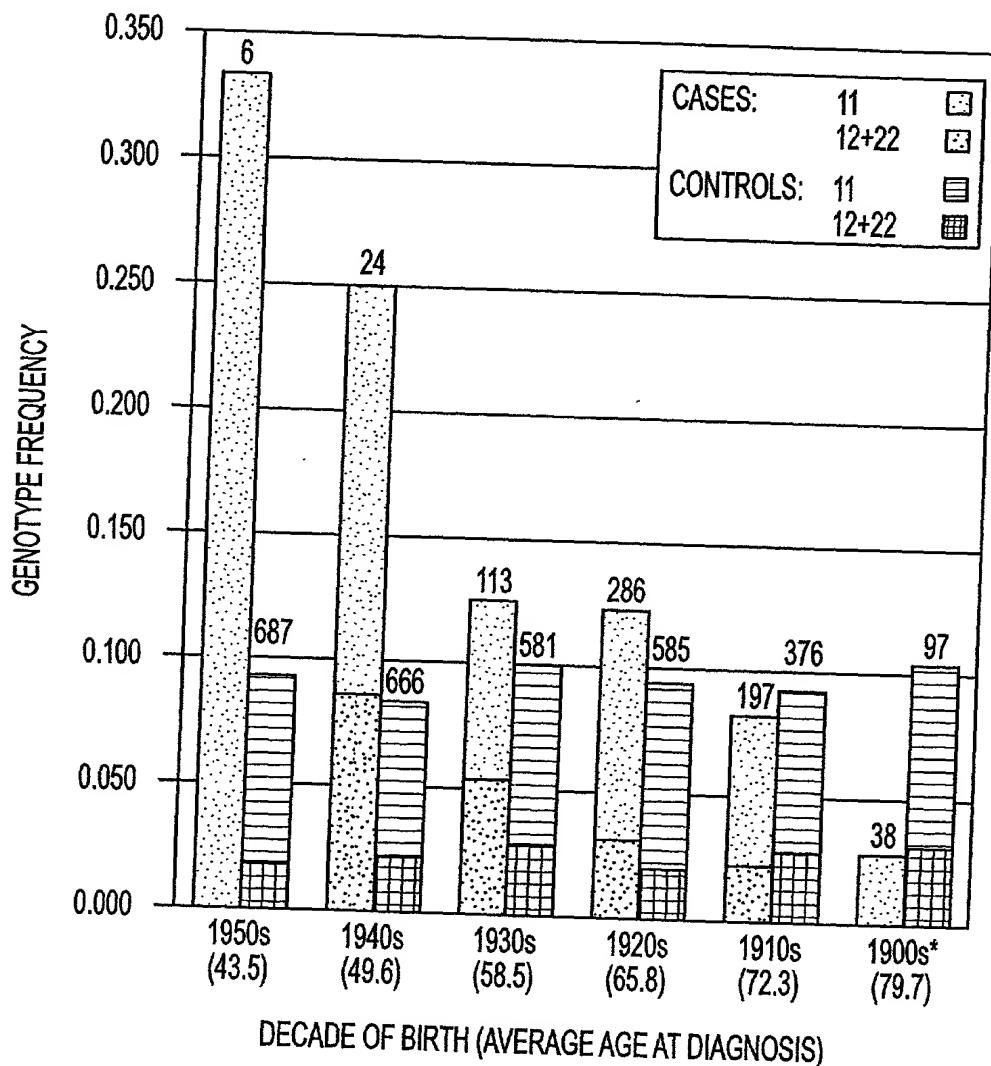


FIG. 7

1920s - 1950s CASES VS. DIVERGENT CONTROLS

		OBSERVED		ODDS RATIO	P-VALUE
		CASES			
00, 01, 02		372	139		
11, 12, 22		57 (13.3%)	9 (6.1%)	2.4	0.026
00, 01, 11		387	143		
02, 12, 22		42 (9.8%)	5 (3.4%)	3.1	0.022
00, 01		347	137		
02, 11, 12, 22		82 (19.1%)	11 (7.4%)	2.9	0.001

1920s - 1950s CASES VS. PEDIGREE UNAFFECTEDS

				ODDS RATIO	P-VALUE
		CASES			
00, 01, 02		372	2151		
11, 12, 22		57 (13.3%)	220 (9.3%)	1.5	0.013
00, 01, 02		372	2151		
11		40 (9.3%)	170 (7.2%)	ODDS RATIO 11	1.4
12, 22		17 (4.0%)	50 (2.1%)	ODDS RATIO 12,22	2.0
				P-VALUE	0.017
				TREND STATISTIC	8.09
				P-VALUE	0.004

FIG. 8

CPSF73 family		
(HSA) CPsf73	1	MSAIPAAEESDQLLIRPLLAGQEVGRSCILLEFKGRKTMILDGCIHPG..LEGMDALPY.IDLDPAED.DLILISHRELDHCGALLPWFQKT
(ATH) gi6751699	1	MASSSTS1KRREQPISRGDQDOLIVTPLAGSEVGRSCVIMSRGKVNILEDGCIIHPA..YSGMAALPY.FDEIDPSSIDVLLTTHEDHAAISLPVPLKFT
(SCE) YSH1	1	MERTNTTTEKFKFS.LGGSNEVGRSCHIQQYKGKTVMLDAGIHPA..YQGLASLPF.YDEFDLISKMDILLISHEHEDHAAISLPVPLKFT
(Syn_sp) gi2496795	1	MTGSVPTQGKAFANISFLPYGGVPRD.GGICIEHLHGPYRILLDCGLED...LTPLLAA.....DPGTVDLVECSHEDHEGIGLWQFHQOF
(Me_t) gi2622312	161	ILQOLGNRIHQPKYDND.WARLTA.MGGEREVGRSCVLYLOTPNSRVLIDCGWNVAGGDDKNSYPYLNVPEFTLDS.DAVVTHAHDHESGFLPYL.YHY

PS02 family  
 (HSA) ha3611  
 (ATH) gi2979557  
 (SCE) PS02

651 KRSDHLIN · TESEAVNLSKWV**KE**TKSA · HGGIQLRGNKKI · PESSIONVGGSRKKT**KE**KKIPGTGFTVDAFQYGVVEGGCTAYPLT**KE**HS  
 350 TANKLITEFFPGQATEGT**KE**TKIRTAPKVAEKSPSDSSSSRAVRRNGNGSKV**KE**PIPHWNCCIPGTFRVDAFKYLTRD · CCEMWELLTHA**KE**ELDEVOGLTKSESHG  
 165 HCDTCIGSDPSSNMGTPKNNI**KE**RSFISNPPSSPAKTKRDIATSKKPTRVK**KE**WLPSSKIIKPFNNGHEIVDGGFNYKASSET**KE**ISQVFLSHTEHSDHYIGLKKSWNNP

ELAC2 family	481	485	466	454
(HSA) ELAC2	...PEIIFLGTGSAIIPWKIRNVSATLVNISP...	...MEIVILGTGSSQPSKVRNVSAIFIDLFS...	...VEIITLGTSALPSKVRNVSTLVKVPFTDA	...DTSLLDCCGGTGFQQL...
(ATH) g16850339	...P...K...I...V...S...A...I...P...W...K...	...M...E...I...V...I...L...G...T...G...S...S...	...V...E...I...I...T...L...G...T...G...S...A...L...	...R...G...S...L...L...D...C...G...E...G...T...F...
(SCE) YKR079C	...P...K...I...V...S...A...I...P...W...K...	...P...K...I...V...S...A...I...P...W...K...	...P...K...I...V...S...A...I...P...W...K...	...P...K...I...V...S...A...I...P...W...K...

CPSF73 family			
(HSA) CPSS73	148	...GIKFWCYHAGHVLGAAWMFIEIA.	...GIVKLLYTGDFSY.
(ATH) gi6751699	158	...GIKFWCYTAGHEVLGAAWMFWDIA.	...GIVRLLYTGDFSY.
(SCE) YSH1	153	...GIKETAFHAGHVLGAAWMFOIEIA.	...GIRVLLYTGDFSY.
(Syn sp) gi2496795	125	...GLTVELLPAAGHLPAGAHLILLEYHNG.	...DRLLYVWITGDFYCLSHLQLVDGLALTPLRGLK.
(Me_f) gi2622312	319	...DIRETILHAGHILGSSAHLHIG.	...DCQIANNVWITGDFR.

PS02 family	(HSA) ha3611	783	...GMKVLLDAHHCPCGAVIILFLYLP...	NGTVIILHTGDFRADPSMERSLLADQK...	...VHMLVYLDITTCSPHYTFPSQQEVIRFAINTAF
(ATH) q12979557	484	...GIDVTCFDDAHHCPCGSIIMLFFEP...	...NGKAVIILHTGDFERYSEEMSNWLIGSH...	...ISSSLVLLDTTTCNPQYDFPKQEAIVQFVVE...	AI
(SCE) PS02	308	...TISWVTLDAHHCPCGAIIMLFEQFLA...	...NSYDKPIRQIILHTGDFERSNAKMIETIQKWL...	...TNTMGYNFSPQHSVCTEVADFTL	

FIG. 9-1

BLAC2 family		
(HSA) BLAC2	634	...LEEFOTCLVRECKHAGCA[VHT.....SGWKKWVYSGDTMP·CEALVRMCK.....DATLILHEATEFEDGLI.....
(ATH) gi6850339	667	...INDLISFPVWECPOAYGVVKAERVNSVGEQILGKWMVYSGDSRP·CPETVEASR.....DATLILHEATEFEDAL.....
(SCE) YKR079C	660	...IEYEQTCAIHCWDAYSNSITFR...MDENNEHNTFKVSYSGDTRPNIEKPSLEIGY.....NSDLILHEATELENQL.....

CPSF73 family		
(HSA) CPSF73	232	...RGGRGLIPVIALGRAOELLILDEYWMNHP...ELH..DIPLY..387 388..VDYISFSAETDQOQSEFIRAI..KPPHVT[VHGEQNEMARLKAA
(ATH) gi6751699	242	...QGRVLLIPAPALGRAOELLILDEWMNHP...DLH..NIPLY..397 398..VHIIISFSAEADYAQSTELKEL..MPPNIIILVHGEANEWMRILKQK
(SCE) YSH1	237	...RGGRVLLIPVRAIGRAOELLILDEYTSQHAD..EIGGGQVPIFY..399 400..VEEISFSAAAEVDEQENLIEEKI..SAPNIIILVHGEANPMGRILKSA
(Syn_sp) gi2496795	216	...KGRNITLIPVPLIGLAQEI[DQI]KJRTTH...QFTGRQVNLMWAA..339 360..LEDYIILADESDGANTQIIHNL..RPOHILVVEHGPQPSDIEDLTSL
(Met_t) gi2622312	407	...RGGGKILIPVFAVGRAQELMIVLEEEYIRTGIIDEVPPVYIDGMWEE..570 571..KTIEGFSSGSDRQ[M]MEYVKRISPKPEKIL[CHGDNYKTIIDLASS

PSO2 family		
(HSA) ha3611	870	...PHALV[CGTY]SICK..EKEV[FLA]ADVLGSKVGMSQEKYKTLOCIN..995 986..IYGIPYSEISSYLEKREVQWL..KPOKIIPTVNVGTVKSRSTME
(ATH) gi2979557	567	...PKTLE[FLIGSY]TICK..ERLFLEVARLREKIVINPAKLKLECLG..605 686..RYEVIPYSEISSSTTELKKEVQKV..SPEVIIIPSVNNNDGPDSAAAMV
(SCE) PS02	433	...YRVLFLV[CGTY]TICK..EKLA[AIK]ICEFLTKLFLVMPNSVFKFSMMIT..602 603..VFNVPYSEISSSPNDIVKGCKL..KCSEVIIPTVNLNLLWKVRYMT

ELAC2 family		
(HSA) ELAC2	.....	.....693 694..EEEAVKETTSITTSQIISVGMRM..NAEFIMIINHFSQR..YAKVPLF
(ATH) gi6850339	.....	.....736 737..IEEALAKNEESTKHEADVGSAA..NVYRIVLTHFSQR..YPKLIPVI
(SCE) YKR079C	.....	.....728 729..LEDAVKKKHCTTNEA[IGVSNK]W..NARKLITTHFSQR..YPKLIPQI

FIG. 9-2

(HSA) ELAC2		(MMU) Elac2		(CEL) CE16965		(ATH) g16850339		(SCE) YKR079C	
%ID	%SIM	%ID	%SIM	%ID	%SIM	%ID	%SIM	%ID	%SIM
100.0	100.0	0.0	0.0	—	—	—	—	—	—
81.6	88.0	1.8	100.0	0.0	—	—	—	—	—
24.2	43.0	14.0	24.6	44.0	15.7	100.0	100.0	0.0	—
25.6	47.0	23.5	25.4	46.0	25.0	21.0	44.0	21.1	—
21.8	41.0	20.8	21.7	43.0	21.4	18.2	43.0	21.4	—
						21.8	41.0	16.3	100.0
								100.0	0.0

FIG. 10

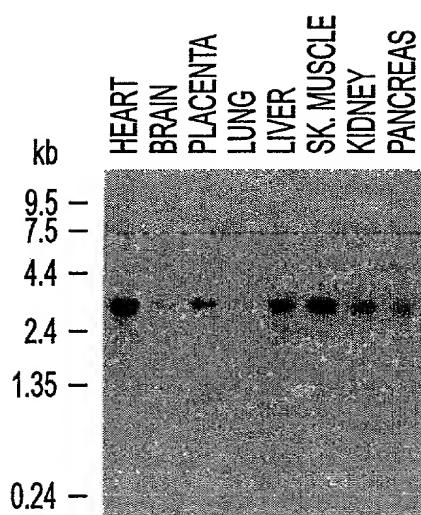


FIG. 11A

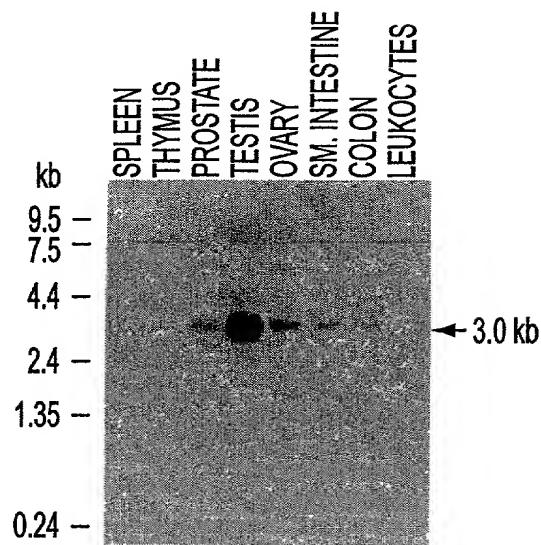


FIG. 11B



FIG. 11C



FIG. 11D

ELAC2, N-terminal sequences

(HSA) ELAC2	52	SGCPNTVYQVVAAGSRDSGAALIVTSEENR...
(MMU) Elac2	44	PGGPNTVYQVVAAGGRDAGAALIVTSEENR...
(CEL) CE16965	87	VNIPSQVSIENVLGN. GTGLLRACFLRTPLK...
(ATH) gi6850339	45	NPTNTIAYAQILGTMDTDQTSSSVLFFDK...
(SCE) YKR079C	1	METFLPITHPTSDTKHPLLLLQSAHGEK...

ELAC2, His motif region

(HSA) ELAC2	475	EKRSQYPEIIFLGTGSAIPMKIRNNVATLNI
(MMU) Elac2	471	EKRSQYPEIIVFLGTGSAIPMEIRNNVSTLN
(CEL) CE16965	480	KMDCCBFPKLTTPFGTSSAVPSKIRNNVIG
(ATH) gi6850339	479	KIRRDDMEIVLIGTGSQPSKIRNNVSAIFDLS
(SCE) YKR079C	460	AEKKKHVEIITLGTGSAALPSKIRNNVSTLKV

ELAC1, N-terminal=His motif region

(HSA) ELAC1	1	MSMDVTFIIGTGAAYPSPTRGASAIVLRC...
(Es_c) elac	1	MKRDELMEIIFLGTISAGVPTTRTRNTAIIINLQHPTQ...
(Syn_sp) gi2500943	1	MEITFLGTSSGVPTRNWISSHAIRLPQ...
(Me_t) gi2622965	1	MMEVTFIIGTSSAVPSKRNHNTSIIAIRP...

FIG. 12

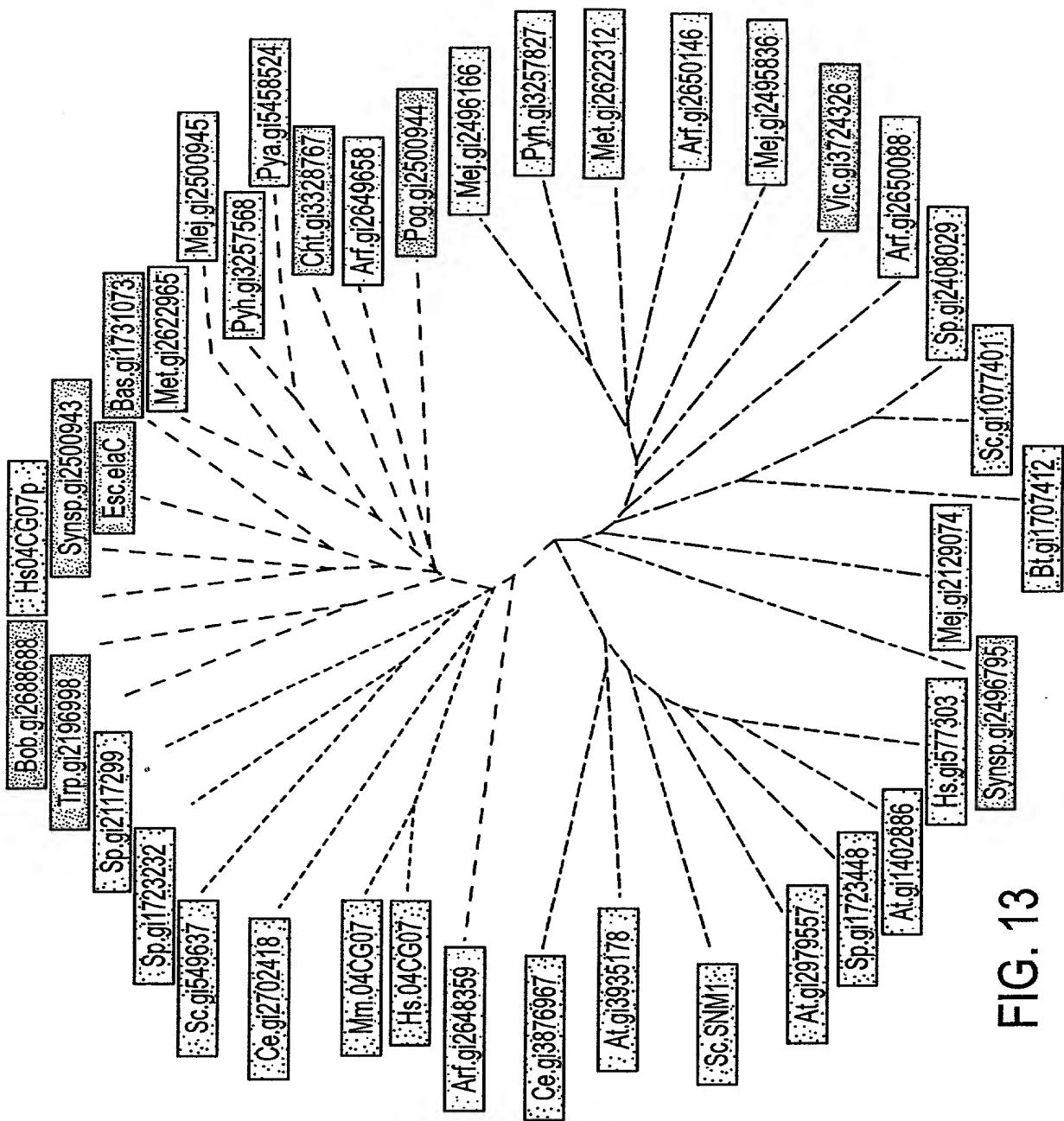


FIG. 13

